1. An isolated nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2; and

b) a nucleic acid molecule which encodes at least 15 contiguous amino acids of SEQ ID NO:2.

2. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

a) the nucleotide sequence of SEQ ID NO:1;

b) the nucleotide sequence of SEQ ID NO:1; wherein all T nucleotides are replaced by U nucleotides;

c) a nucleotide sequence complementary to (a) or (b); and

d) a fragment of (a), (b), or (c) that is at least 25 nucleotides in length.

3. An isolated nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule which encodes a polypeptide that is at least 80% identical to SEQ ID NO:2;

b) a nucleic acid molecule which hybridizes under stringent conditions to a nucleic acid molecule having the sequence of SEQ ID NO:1; and

c) a nucleic acid molecule which hybridizes under stringent conditions to a nucleic acid having the cDNA sequence contained within ATCC Accession No. _____.

4. A substantially pure polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2; and

b) a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:2.

5. The polypeptide of claim 4, wherein the polypeptide is fused to a heterologous polypeptide.

6. A substantially pure polypeptide selected from the group consisting of:

a) a polypeptide encoded by a nucleic acid molecule which hybridizes under stringent conditions to the nucleic acid molecule of SEQ ID NO:1;

b) a polypeptide encoded by a nucleic acid molecule that hybridizes under stringent conditions to the cDNA sequence contained within ATCC Accession No. _____.

7. The polypeptide of claim 6, wherein the polypeptide is fused to a heterologous polypeptide.

8. A method for detecting the presence of a nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2;

b) a nucleic acid molecule which encodes at least 15 contiguous amino acids of SEQ ID NO:2;

in a sample, the method comprising the steps of:

i) contacting the sample with a nucleic acid probe which selectively hybridizes to the nucleic acid molecule; and

ii) determining whether the nucleic acid probe binds to the nucleic acid molecule in the sample.

9. The method of claim 8, wherein the sample comprises mRNA.

10. A method for producing a substantially pure polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2; and

b) a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:2;

the method comprising the step of culturing a host cell containing the nucleic acid molecule encoding the polypeptide under conditions in which the nucleic acid molecule is expressed.

11. The method of claim 10, wherein the host cell is a bacterium.

12. A method for detecting the presence of a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2; and

b) a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:2;

in a biological sample, the method comprising the steps of:

i) contacting the sample with a compound which selectively binds to the polypeptide; and

ii) determining whether the compound binds to the polypeptide in the sample.

13. The method of claim 12, wherein the compound which binds to the polypeptide is an antibody.

14. A method for identifying a compound which binds to a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2; and

b) a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:2;

the method comprising the steps of:

i) contacting the polypeptide with a test compound; and

ii) determining whether the polypeptide binds to the test compound.

15. The method of claim 14, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

a) direct detection of the binding; and

b) detection of a competitor molecule which disrupts binding of the test compound to the polypeptide.

16. A method for modulating the activity of a polypeptide selected from:

a) a polypeptide comprising having amino acid sequence of SEQ ID NO:2; and

b) a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:2;

the method comprising contacting a cell expressing the polypeptide with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

17. The method of claim 16, wherein the activity is recruitment of a caspase.

18. The method of claim 16, wherein the method results in an increase in hexose uptake by the cell.

19. The method of claim 16, wherein the method results in a decrease in hexose uptake by the cell.

20. A method of identifying a compound that modulates the expression of a gene encoding GLUTX, the method comprising the steps of:

a) contacting a cell expressing a gene with a test compound; and

b) detecting the level of expression of the gene in the presence of the test compound, wherein a difference in expression in the presence of the test compound compared to expression in the absence of the test compound indicates that the test compound modulates expression of the gene.

21. The method of claim 20, wherein the compound is selected from the group consisting of polypeptides, ribonucleic acids, small molecules, ribozymes, antisense oligonucleotide, and deoxyribonucleic acids.

22. A method of identifying a compound that modulates the activity of GLUTX, the method comprising the steps of:

a) contacting the polypeptide with a test compound; and

b) detecting the level of activity of GLUTX having the amino acid sequence of SEQ ID NO:2 in the presence of the test compound, wherein a difference in activity in the presence of the test compound compared to the activity in the absence of the test compound indicates

that the test compound modulates the activity of GLUTX.

23. The method of claim 22, wherein the compound is selected from the group consisting of polypeptides, ribonucleic acids, small molecules, ribozymes, antisense oligonucleotides, and deoxyribonucleic acids.

24. A method for modulating hexose uptake, the method comprising modulating the expression or activity of a gene encoding the amino acid sequence of SEQ ID NO:2.

25. A method for treating a patient having a disorder associated with aberrant expression or activity of a gene encoding the amino acid sequence of SEQ ID NO:2, the method comprising administering a therapeutically effective amount of a compound that decreases the expression or activity of the gene.

26. The method of claim 25, wherein the compound is selected from the group consisting of polypeptides. ribonucleic acids, small molecules, ribozymes, antisense oligonucleotides, and deoxyribonucleic acids.

27. A method for treating a patient having a disorder associated with aberrant expression or activity of a GLUTX polypeptide comprising the amino acid sequence of SEQ ID NO:2, the method comprising administering a therapeutically effective amount of a compound that increases the expression or activity of the gene.

28. The method of claim 27, wherein the compound is selected from the group consisting of polypeptides, ribonucleic acids, small molecules, ribozymes, antisense

oligonucleotides, and deoxyribonucleic acids.

29. A method for diagnosing a patient as having a disorder associated with aberrant expression of GLUTX, comprising measuring expression of a GLUTX polypeptide having the sequence of SEQ ID NO:2 in a biological sample obtained from the patient, wherein increased or decreased GLUTX expression in the biological sample, compared with GLUTX expression in a control sample, indicates that the patient has a disorder associated with aberrant expression of GLUTX.

30. A method for diagnosing a patient as having a disorder associated with expression of an isoform of GLUTX, comprising isolating GLUTX mRNA or GLUTX polypeptide from the patient and determining the sequence of the mRNA or polypeptide, a difference in the sequence, as compared to the nucleotide sequence of SEQ ID NO:1 or the polypeptide sequence of SEQ ID NO:2, respectively, indicating expression of an isoform of GLUTX.

31. A method for diagnosing a patient as having a disorder associated with aberrant activity of GLUTX, comprising measuring the activity of a GLUTX polypeptide having the amino acid sequence of SEQ ID NO:2 in a biological sample obtained from the patient, wherein increased or decreased GLUTX activity in the biological sample, compared with GLUTX activity in a control sample, indicates that the patient has a disorder associated with aberrant activity of GLUTX.

32. The method of claim 20, wherein the gene further comprises a sequence encoding an amino acid sequence

selected from the group consisting of:

i) the amino acid sequence of SEQ ID NO:2, and

ii) at least 15 contiguous amino acids of SEQ ID NO:2.